Snake venomics of the South and Central American bushmasters. Comparison of the toxin composition of *Lachesis muta* gathered from proteomic versus transcriptomic analysis

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We report the proteomic characterization of the venoms of two closely related pitvipers of the genus *Lachesis*, *L. muta* and *L. stenophrys*, and compare the toxin repertoire of the former revealed through a proteomic versus a transcriptomic approach. The protein composition of the venoms of *L. muta* and *L. stenophrys*, analyzed by a snake venomics approach, comprised 30-40 proteins of molecular masses in the range of 13-110 kDa and belonging, respectively, to only 8 and 7 toxin familiies in *L. muta* and *L. stenophrys* venoms. Both venoms contained a large number of bradykinin-potentiating peptides and a C-type natriuretic peptide, which comprised around 15% of the total venom proteins. In both species, the most abundant proteins were Zn^{2+}-metalloproteinases (32-38%) and serine proteinases (25-31%), followed by PLA_2s (9-12%), galactose-specific C-type lectin (4-8%), L-amino acid oxidase (LAO, 3-5%), CRISP (1.8%; found in *L. muta* but not in *L. stenophrys*), and NGF (0.6%). On the other hand, only six *L. muta* venom secreted proteins matched any of the previously reported 11 partial or full-length venom gland transcripts, and venome and transcriptome depart in their relative abundances of different toxin families. As expected from their close phylogenetic relationship, the venoms of *L. muta* and *L. stenophrys* share (or contain highly similar) BPPs, serine proteinases, a galactose-specific C-type lectin, and LAO. However, they dramatically depart in their PLA_2s. Intraspecific quantitative and qualitative differences in the expression of PLA_2 molecules were found in the venoms of five *L. muta* specimens (3 from Bolivia and 2 from Peru) and an *L. muta* venom purchased from Sigma. These observations indicate that these class of toxins represents a rapidly-evolving gene family, and suggests that functional differences due to structural changes in PLA_2s molecules among these snakes may have been a hallmark during speciacion and adaptation of diverging snake populations to new ecological niches, or competition for resources in existing ones. Our data may contribute to a deeper understanding of the biology and ecology of these snakes, and may also serve as a starting point for studying structure-function correlations of individual toxins.